

Study Examines, Compares Bacteria in the Nose and Throat

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Scientists have completed the most comprehensive comparative analysis to date of bacterial communities inhabiting the human nose and throat, which could provide new insights into why some individuals become colonized with pathogens while others do not. They release their findings today in mBio™ the online open-access journal published by the *American Society for Microbiology*.

"The nose and throat are important sites of pathogen colonization, yet the microbiota of both are relatively unexplored by culture-independent approaches," says Katherine Lemon of Children's Hospital Boston, a lead author on the study that also included researchers from Harvard Medical School, Lawrence Berkeley National Laboratory and the University of California, San Francisco.

Until now most of the knowledge of bacteria living in the nose and throat has been generated using culture-based techniques and has primarily focused on identifying pathogenic bacteria. In this study, Lemon and her colleagues examined and compared the bacterial communities from the noses and throats of seven healthy adults using two different culture-independent methods one of which was a 16S rRNA microarray, called the PhyloChip, which possesses 500,000 probes and can detect approximately 8,500 different genetically distinct groups of bacteria.

Despite the close physical connection between the nose and throat, the researchers found distinct differences in bacterial populations. In the nose the majority of bacteria found were of the phyla Firmicutes and Actinobacteria and compared to other areas of the body that had been studied the distribution was most reminiscent of the skin. In the throat the majority of bacteria were of the phyla Firmicutes, Proteobacteria and Bacteroidetes and the distribution was more similar to that found in saliva.

They also found an inverse relationship between the prevalence of the Staphylococcaceae family of bacteria, whose members include important pathogens like *Staphylococcus aureus*, and Corynebacteriaceae and Propionibacteriaceae families, whose members are more commonly benign commensals.

"This survey of the microbiota of the nostril and oropharynx from seven healthy adults contributes to the growing understanding of the composition of healthy human microbiota and its interpersonal variation. An improved understanding of competitive bacterial colonization will increase our ability to define predispositions to pathogen carriage at these sites and the subsequent risk of infection," says Lemon.